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SEQUENCE LISTING

<110> Yu, Guo-Liang
Ni, Jian
Rosen, Craig A.

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<140> 09/246,129

<141> 1999-02-08

<150> 60/074,047

<151> 1998-02-09

<150> 09/131,237

<151> 1998-08-07

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<150> 08/461,246

<151> 1995-06-05

<150> PCT/US94/12880

<151> 1994-11-07

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 Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly
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 Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys
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 Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly
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Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
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Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
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Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
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 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
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 130 135 140
 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
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 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
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 Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
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 Arg Arg Gln Gly Tyr Gly Pro Leu Trp Tyr Thr Ser Val Gly Phe Gly
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 Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg
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 Glu Phe Thr Asn His Ser Leu Arg Val Ser Ser Phe Glu Lys Gln Ile
 115 120 125
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 His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro Leu Glu Trp Glu
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 Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val
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 Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu Ser His Lys Val
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Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val Leu Met Glu Glu
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gaagataaaa ccttcttttg agccttctta ctataggagg agagcaaata tcattatatg 240

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 gggaatgaac ctctgaantg ccagtgaata tcagncaagc aggccgacca aacaagccag 180
 antccatnca ctgtggtcat caccaaggta acagacagct accctgagcc aaccagctc 240
 cttcatgggg accaagtttg tttgcgaant aggttagcaa ctggttccag cccattttac 300
 cttggggggc agttctnctt gncaagaagg ggacaagctt atggtggaac gttcatanca 360
 tcnttttttg gtggntttac acaaaagg 388

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<210> 14
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<210> 16
 <211> 36
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<400> 16
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<210> 17
 <211> 56

<212> DNA
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<212> DNA
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tctcccgga tcttgaggtc acatgcgtgg tggtaggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcagg tctccaacaa agcctccca acccccatcg 360
agaaaacat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ctttcttct ctacagcaag ctacaccgtg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
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gactctagag gat 733

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ctggtgttgc tccccttct tgcaggactc accacatacc tgcttgtag ccagctccgg 180
gcccagggag aggcctgtgt gcagttccag gctctaaaag gacaggagtt tgcaccttca 240
catcagcaag tttatgcacc tcttagagca gacggagata agccaagggc acacctgaca 300
gttgtgagac aaactccac acagcacttt aaaaatcagt tcccagctct gactgggaa 360
catgaactag gcctggcctt caccaagaac cgaatgaact ataccaacaa attcctgctg 420
atcccagagt cgggagacta cttcatttac tcccaggta cattccgtgg gatgacctct 480

gagtgcagtg aaatcagaca agcaggccga ccaaacaagc cagactccat cactgtggtc 540
 atcaccaagg taacagacag ctaccctgag ccaaccagc tcctcatggg gaccaagtct 600
 gtatgcgaag taggtagcaa ctggttccag cccatctacc tcggagccat gttctccttg 660
 caagaagggg acaagcta at ggtgaacgtc agtgacatct ctttggtgga ttacacaaaa 720
 gaagataaaa ctttcttttg agccttctta ctataggagg agagcaaata tcattatatg 780
 aaagtcctct gccaccgagt tcctaatttt ctttggtcaa atgtaattat aaccaggggt 840
 tttcttgggg cggggagtag gggcattcca cagggacaac ggttttagcta tgaaatttgg 900
 ggcccaaaat ttcacacttc atgtgcctta ctgatgagag tactaactgg aaaaaggctg 960
 aagagagcaa atatattatt aagatgggtt ggaggattgg cgagtttcta aatattaaga 1020
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 Ala Arg Trp Ala Leu Thr Cys Cys Leu Val Leu Leu Pro Phe Leu Ala
 35 40 45
 Gly Leu Thr Thr Tyr Leu Leu Val Ser Gln Leu Arg Ala Gln Gly Glu
 50 55 60
 Ala Cys Val Gln Phe Gln Ala Leu Lys Gly Gln Glu Phe Ala Pro Ser
 65 70 75 80
 His Gln Gln Val Tyr Ala Pro Leu Arg Ala Asp Gly Asp Lys Pro Arg
 85 90 95
 Ala His Leu Thr Val Val Arg Gln Thr Pro Thr Gln His Phe Lys Asn
 100 105 110
 Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu Ala Phe Thr
 115 120 125
 Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile Pro Glu Ser
 130 135 140
 Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly Met Thr Ser
 145 150 155 160
 Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys Pro Asp Ser
 165 170 175

Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro Glu Pro Thr
180 185 190

Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly Ser Asn Trp
195 200 205

Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln Glu Gly Asp
210 215 220

Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp Tyr Thr Lys
225 230 235 240

Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
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<211> 434

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caagaagggg acnagctaag ggtgaacgac agtgacatct ctttggtgga ttacacaaaa 180

gaagataaaa ccttcttttg agccttctta ctataggagg agagcaaata tcattatatg 240

aaagtctctt gccaccgagt tcctaatttt ctttggtcaa atgtaattat aaccaggggt 300

tttcttgggg cggggagtag ggggcattcc cacagggaca acggttttagc tatgaaattt 360

ggggggccca aaatttcaca acttcatngt tgcccttact tgatgagaag tacttaactt 420

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434

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nnnttnnaat gctgccagag cacggcagct gcaggcccaa ggccaggagc agcagcgcac 120

gctgggctct cacctgctgc ctggtgttgc tccccttctt tgcaggactc accacatacc 180

tgcttgtcag ccagcttcgg gnccagggng aggctgtgt gcagttccag ggtctaaaag 240

gacaggagtt tgcaccttca catcagcaag tttatgcacc tnttagagca gacggagata 300

agccangggg acaactgaca nttgtgagac aaattccaca cagnanttta aaatcagttt 360

ccagttttga atggggacan nattaggctg gcttnacaag accgntggat tttacag 417

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gggaatgaac ctctgaantg ccagtgaaaa tcagncaagc aggccgacca aacaagccag 180
antccatnca ctgtgggtcat caccaaggta acagacagct accctgagcc aaccagctc 240
cttcatgggg accaagtttg tttgcgaant aggttagcaa ctggttccag cccattttac 300
cttggggggc agttctnctt gncaagaagg ggacaagctt atggtggaac gttcatanca 360
tcnttttttg gtggnTTT acaaaagg 388

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<212> DNA
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cccaaaatth cacacttcat gtgccttact gatgagagta ctaactggaa aaaggctgna 120
agagagcaaa tatattatta agatggggttg gaggattggc gagtttctaa atattaagac 180

actggatcac tgaaatgaat ggatgatcta ctgggtcca ggattgaaag agaaatattt 240
caacaccttc ctgctataca atggtcacca gtggtccagt tattgttcca atttgatcc 300
atnaatttgc nttcaattcc aggagctttg gaaggaattc caaggaaagc tccaggaaaa 360
cgtattaaa ctttcaggg gccaaantcc ttcaccaatt tttccacna actttccagg 420
cctgncncaa aaaaatggaa agggagttgg tangtccc 458